CLAIMS

What is claimed is:

1. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) an amino acid sequence which is at least 85% identical to the amino acid sequence set forth in SEQ ID NO:3;

(b) an amino acid sequence encoded by a nucleic acid comprising a nucleotide sequence set forth in SEQ ID NO:2; and

(c) an amino acid sequence encoded by a nucleic acid which specifically hybridizes under stringent conditions to either strand of a denatured, double-stranded nucleic acid comprising a nucleotide sequence set forth in SEQ ID NO:2.

2. An isolated polypeptide according to claim 1 wherein said isolated polypeptide has secondary metabolite gene cluster regulating activity.

3. An isolated polypeptide according to claim 1 wherein said polypeptide regulates the activity of a lovastatin or penicillin biosynthesis gene cluster.

4. An isolated polypeptide according to claim 1 wherein said isolated polypeptide has protein methyltransferase activity.

5. An isolated polypeptide according to claim 1 comprising an amino acid sequence at least 95% identical to the amino acid sequence set forth in SEQ ID NO:3.

6. An isolated polypeptide according to claim 1 comprising an amino acid sequence set forth in SEQ ID NO:3.

7. An isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence set forth in SEQ ID NO:2;

(b) a nucleotide sequence encoding an amino acid sequence set forth in SEQ ID NO:3; and

(c) a nucleotide sequence which specifically hybridizes under stringent conditions to either strand of a denatured, double-stranded nucleic acid having a nucleotide sequence set forth in SEQ ID NO:2.

8. An isolated nucleic acid according to claim 7 wherein said isolated nucleic acid encodes a polypeptide having secondary metabolite gene cluster regulating activity.

9. An isolated nucleic acid according to claim 7 wherein said isolated nucleic acid regulates the activity of a lovastatin or penicillin biosynthesis gene cluster.

10. An isolated nucleic acid according to claim 6 wherein said isolated nucleic acid encodes a polypeptide having protein methyltransferase activity.

11. An expression vector comprising an isolated nucleic acid according to claim 7 wherein said isolated nucleic acid is in operative association with one or more regulatory elements.

12. A transformed host cell or organism comprising an isolated nucleic acid according to claim 7.

13. A transformed host cell or organism according to claim 12 wherein said transformed host cell is capable of at least a two fold increase in production of a secondary metabolite relative to non-transformed cells or organisms.

14. A method of preparing an isolated polypeptide comprising LaeA or fragments thereof, comprising the step of culturing a transformed host cell or organism of claim 12 under conditions conducive to expression of the polypeptide, and recovering the expressed polypeptide from the cell or organism in isolated form.

15. A method of detecting a nucleic acid encoding an amino acid sequence set forth in SEQ ID NO:3 in a biological sample comprising the steps of:

(a) hybridizing a complement of a nucleotide sequence which encodes an amino acid sequence as set forth in SEQ ID NO:3 to a nucleic acid material of a biological sample thereby forming a hybridization complex; and

(b) detecting the hybridization complex wherein the presence of the complex correlates with the presence of a nucleic acid encoding an amino acid sequence set forth in SEQ ID NO:3.

16. A method of increasing the amount of a secondary metabolite produced in a cell or organism, comprising the steps of:

(a) obtaining a cell or an organism capable of biosynthesizing a secondary metabolite;

(b) transforming said cell or organism with a nucleic acid according to claim 8; and

(c) culturing said transformed cell or organism so that an increase in production of the secondary metabolite occurs in the transformed cell or organism as compared to a non-transformed cell or organism.

17. A method according to claim 16 wherein said cell or organism is an *Aspergillus* species.

18. A method according to claim 17 wherein the *Aspergillus* species is *A. nidulans or A. terreus.*

19. A method according to claim 17 wherein the secondary metabolite is lovastatin or penicillin.

20. A method according to claim 16 wherein said nucleic acid according to claim 8 overexpresses a polypeptide having secondary metabolite gene cluster regulating activity.

21. A method of decreasing the production of a secondary metabolite in a transformed cell or organism, comprising the steps of:

(a) obtaining a transformed cell or organism capable of biosynthesizing a secondary metabolite, said transformed cell or organism having a defective *laeA* gene

wherein the defective *laeA* gene is no longer biologically active and expression of secondary metabolite gene clusters is reduced; and

(b) culturing said transformed cell or organism so that a decrease in production of the secondary metabolite occurs in the transformed cell or organism as compared to a non-transformed cell or organism.

22. A method according to claim 21 wherein the transformed cell or organism is *A. parasiticus* or *A. flavus.*

23. A method of producing an isolated secondary metabolite, comprising steps of:

(a) obtaining a cell or an organism capable of biosynthesizing a secondary metabolite;

(b) transforming said cell or organism with a nucleic acid according to claim 8;

(c) culturing said transformed cell or organism under conditions conducive to increasing production of the secondary metabolite in the transformed cell or organism as compared to a non-transformed cell or organism; and

(d) recovering said secondary metabolite from the transformed cell or organism in an isolated form.

24. A method according to claim 23 wherein said cell or organism is an *Aspergillus* species.

25. A method according to claim 24 wherein the *Aspergillus* species is *A. nidulans* or *A. terreus*.

26. A method according to claim 24 wherein the secondary metabolite is lovastatin or penicillin.

27. A method according to claim 23 wherein said nucleic acid according to claim 8 overexpresses a polypeptide having secondary metabolite gene cluster regulating activity.

28. A method for identifying a novel secondary metabolite biosynthesis gene cluster in a fungus, said method comprising steps of:

(a) obtaining a transformed fungus having a disrupted *laeA* gene;

(b) isolating a sample of nucleic acids from the transformed fungus of step (a), said sample of nucleic acids representative of the expressed genes of the transformed fungus;

(c) hybridizing the sample of nucleic acids isolated in step (b) or nucleic acid equivalents of same with an array comprising a plurality of nucleic acids representative of the expressed genes of a non-transformed fungus under conditions to form one or more hybridization complexes;

(d) detecting said hybridization complexes;

(e) comparing the levels of the hybridization complexes detected in step (c) with the level of hybridization complexes detected in a sample of nucleic acids isolated

from an *laeA*-expressing fungus and representative of the expressed genes of the *laeA*-expressing fungus, wherein an altered level of hybridization complexes detected in step (c) compared with a level of hybridization complexes of the sample of nucleic acids from the *laeA*-expressing fungus correlates with and identifies at least one gene under regulatory control of the *laeA* gene product; and

(f) examining genomic nucleotide sequence surrounding said gene identified in step (e) to determine if said gene is clustered with secondary metabolite biosynthesis genes thereby identifying a novel secondary metabolite biosynthesis gene cluster.

29. A method according to claim 28, wherein said nucleic acids representative of the expressed genes of the non-transformed fungus in step (c) are immobilized on a substrate.

30. A method according to claim 28, wherein said said nucleic acids representative of the expressed genes of the non-transformed fungus in step (c) are hybridizable elements in a microarray.

31. A method according to claim 28, wherein the sample of nucleic acids isolated from the *laeA*-expressing fungus and representative of the expressed genes of the *laeA*-expressing fungus in step (e) are isolated from a transformed fungus overexpressing *laeA* gene product as compared to the non-transformed fungus.

32. A method according to claim 28 wherein the fungus is an *Aspergillus* or *Fusarium* species.